

FIGURE 19

CAGTCACCATGAAGCTGGGCTGTGTCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG
CTCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTGTAGACGCTGCAGTGTGAGGGACCTGT
CTGCACCTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT
TCCAGGTCAAGGCCTACACTTTTCAGTGAACCCCTTCCACCTGATTGTGTCTATGACTGGCTG
ATCCTCCAAGGTCAGCCAAGCCAGTTTTTGAAGGGGACCTGCTGGTCTGCGCTGCCAGGC
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTTACCGAGATGGCTCAGCTCTGGGTCCCC
CGGGGCTTAACAGGGAATTTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC
TGCAGTGGCATCTTTCAGAGCCCTGGTCTGGGATCCAGAAACAGCATCTGTGTGGCTAT
CACAGTCCAAGAACTGTTTCCAGCGCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG
CAGGAAGCCCCATGACCTGAGTTGTGAGACAAAGTTGCCCTGCAGAGGTGAGCTGCCCGC
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCACTCGGTGTGAGGCAGCCACTGAGG
ACAACCAAGTTTGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT
GCTGCACCTCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAATGCTCCTGA
GGAGGCCCCCTGGGCTCTGCCTCCGCGGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATG
CAGGATGTGAGAGTCTCTCCTCGGTACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA
GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAAGTAAACAGTTTCATCCATGATCTCACT
TAACCAACCCCAATAAATCTGATTCTTTATTTTCTCTTCTGCTCCTGCACATATGCATAAGTA
CTTTTACAAGTTGCTCCAGTGTTTTGTTAGAATAATGTAGTTAGGTGAGTGTAATAAATTT
ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTTTAACACAAACAGAATTC
TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAA
CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACA
TTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGGGGGTGGGGGATGGTGGGATGT
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCTTATAATGCACAG
GGCAGTACCCCAACAGAAAAATAATCTGGCCCAAAATGTGAGTTGTACTGAGTTTGAGAAA
CCCCAGCCTAATGAAACCCCTAGGTGTGGGCTCTGGAATGGGACTTTGTGCCCTTCTAATTAT
TATCTCTTCCAGCCTCATTAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGTATG
GTCTGTTCTTTAGTTCTAGTTTGTATCCCCTCAAAGCCATTATGTTGAATCCTAATCCC
AAGGTATGGCATTAGAAGTGGGCCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC
ATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCTTCCACCAT
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAACAGCTGTCGCCAAACACCG
ACTCTGTCTGTGCCTTGATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAAATTTCTGG
TGTGTTGTAGCCTAA

0978295-104501

FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594
><subunit 1 of 1, 359 aa, 1 stop
><MW: 38899, pI: 5.21, NX(S/T): 0
MKLGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESCHTEDDLTDAREAGFQV
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRCAWQDWPLTQVTFFYRDGSALGPPGP
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS
PMTLSCQTKLPLQRSAAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ
VWKQSPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAPPEAPGPLPPPPPTPSSSEDPGFSSPL
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

00078295-10-1501

FIGURE 21

CCCACGCGTCCGCCACGCGTCCGCCACGGGTCCGCCACGCGTCCGGGCCACCAGAAGTT
 TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG
 ATCTTACTGGGCCCTGCTACTCTCTGGGGCACCTAACAGTGGACACTTATGGCCGCTCCCATCCT
 GGAAGTGCCAGAGAGTGTAAACAGGACCTTGGAAGAGGGGATGTGAATCTTCCCTGCACCTATG
 ACCCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCCT
 GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAGTACCAGGGCCG
 CTGCGATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCTTGGAGATGG
 ATGACCGGAGCCACTACACGTGTGAAGTCACTGGCAGACTCCTGATGGCAACCAAGTCGTG
 AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCACAGTGACAAC
 TGGCAGCGGTTATGGCTTCACGGTGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC
 GGGGTTCTCCTCCATCAGTTTATTTGGTATAAGCAACAGACTAATAACAGGAAACCCATC
 AAAGTAGCAACCCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA
 TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG
 TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC
 TTGAAAGCAACATCTACAGTGAAGCAGTCTCTGGGACTGGACCACTGACATGGATGGCTACCT
 TGGAGAGACCACTGCTGGGCCAGGAAAGAGCCTGCCTGTCTTTGGCCATCATCTCATCATCT
 CCTTGTGCTGTATGGTGGTTTTTACCATGGCCCTATATCATGCTCTGTCCGAAGACATCCCAA
 CAAGAGCATGTCTACGAAGCAGCCAGGTAAAGAAAGTCTCTCCTCTTCCATTTTTGACCCCGT
 CGCTGCCCTCAATTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCACAGACCC
 AATCCTAAGGCCGGAGGCCCTTCAAGGTCAAGACATAGCTGCCTTCCCTCTCTCAGGCACCTT
 CTGAGTTGTTTTGGCCCTCTGAACACAAAGGATAATTAGATCCATCTGCCTTCTGCTTCC
 AGAATCCCTGGGTGGTAGGATCTTGATAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA
 AACCAGGACCAAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA
 TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATTTCCGCAAGTGGCTGCT
 CCAGTGATGAGCCAACTTCCAGAACTCTGGGCAACAACACTACTCTGATGAGCCCTGCATAGGA
 CAGGAGTACCAGATCATCGCCAGATCAATGGCAACTACGCCCGCCTGTGGACACAGTTCC
 TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTTAAAAATGCCCATTAGGC
 CAGGATCTGCTGACATAATTGCTAGTCAGTCTTGGCTTCTGATGGCTTCTTCTCCTGTCT
 ACCTCTCTTCTGGATAGCCAAAGTGTCCGCTACCAACACTGGAGCCGCTGGGAGTCACT
 GGCTTTGGCCCTGGAAATTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTGGCTCTGG
 GCCCTTCTAGTATCTCTGCGGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGGAAGATG
 CCCATAGCACTAGGACTTGGTCATCATGCTTACAGACACTATTCAACTTTGGCATCTTGCCA
 CCAGAAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT
 TTCTCTTTCTTCAAGGCCAGACAGCTTTTAATTGAATTTGTTATTTACAGGCCAGGGTTCA
 GTTCTGCTCCTCCACTATAAGTCTAATGTCTGACTCTCTCCTGGTGTCAATAAATATCTA
 ATCATAACAGC

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